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**RAW SEQUENCE LISTING
PATENT APPLICATION US/08/713,928A**DATE: 12/31/96
TIME: 10:33:19**INPUT SET: S14725.raw**

This Raw Listing contains the General Information Section and up to the first 5 pages.

1 **SEQUENCE LISTING**
2
3 (1) General Information:
4
5 (i) APPLICANT: RADIN, DAVID N.
6 CRAMER, CAROLE L.
7 OISHI, KAREN K.
8 WEISSENBORN, DEBORAH L.
9
10 (ii) TITLE OF INVENTION: PRODUCTION OF LYSOSOMAL ENZYMES IN
11 PLANT-BASED EXPRESSION SYSTEMS
12
13 (iii) NUMBER OF SEQUENCES: 12
14
15 (iv) CORRESPONDENCE ADDRESS:
16 (A) ADDRESSEE: Pennie & Edmonds
17 (B) STREET: 1155 Avenue of the Americas
18 (C) CITY: New York
19 (D) STATE: New York
20 (E) COUNTRY: USA
21 (F) ZIP: 10036-2711
22
23 (v) COMPUTER READABLE FORM:
24 (A) MEDIUM TYPE: Floppy disk
25 (B) COMPUTER: IBM PC compatible
26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
28
29 (vi) CURRENT APPLICATION DATA:
30 (A) APPLICATION NUMBER:
31 (B) FILING DATE:
32 (C) CLASSIFICATION:
33
34 (vii) PRIOR APPLICATION DATA:
35 (A) APPLICATION NUMBER: US 60/003,737
36 (B) FILING DATE: 14-SEP-1995
37
38 (viii) ATTORNEY/AGENT INFORMATION:
39 (A) NAME: Coruzzi, Laura A.
40 (B) REGISTRATION NUMBER: 30,742
41 (C) REFERENCE/DOCKET NUMBER: 7956-0011-999
42
43 (ix) TELECOMMUNICATION INFORMATION:
44 (A) TELEPHONE: (212) 790-9090
45 (B) TELEFAX: (212) 869-9741
46 (C) TELEX: 66141 PENNIE**ENTERED**

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47

48

49 (2) INFORMATION FOR SEQ ID NO:1:

50

51 (i) SEQUENCE CHARACTERISTICS:

52 (A) LENGTH: 27 base pairs
53 (B) TYPE: nucleic acid
54 (C) STRANDEDNESS: single
55 (D) TOPOLOGY: unknown

56

57 (ii) MOLECULE TYPE: other nucleic acid

58 (A) DESCRIPTION: /desc = "PCR primer"

59

60

61

62

63 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

64

65 TTGTCTAGAG TAAGCATCAT GGCTGGC

27

66

67 (2) INFORMATION FOR SEQ ID NO:2:

68

69 (i) SEQUENCE CHARACTERISTICS:

70 (A) LENGTH: 33 base pairs
71 (B) TYPE: nucleic acid
72 (C) STRANDEDNESS: single
73 (D) TOPOLOGY: unknown

74

75 (ii) MOLECULE TYPE: other nucleic acid

76 (A) DESCRIPTION: /desc = "PCR primer"

77

78

79

80

81 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

82

83 CACGAATTCT GGCGACGCCA CAGGTAGGTG TGA

33

84

85 (2) INFORMATION FOR SEQ ID NO:3:

86

87 (i) SEQUENCE CHARACTERISTICS:

88 (A) LENGTH: 1642 base pairs
89 (B) TYPE: nucleic acid
90 (C) STRANDEDNESS: unknown
91 (D) TOPOLOGY: unknown

92

93 (ii) MOLECULE TYPE: cDNA

94

95

96

97

98 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

99

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100	ATGGAGTTT CAAGTCCTTC CAGAGAGGAA TGTCCCAAGC CTTTGAGTAG GGTAAGCATC	60
101		
102	ATGGCTGGCA GCCTCACAGG TTTGCTTCTA CTTCAGGCAG TGCGTGGGC ATCAGGTGCC	120
103		
104	CGCCCCCTGCA TCCCTAAAAG CTTCGGCTAC AGCTCGGTGG TGTGTGTCTG CAATGCCACA	180
105		
106	TACTGTGACT CCTTTGACCC CCCGACCTTT CCTGCCCTTG GTACCTTCAG CCGCTATGAG	240
107		
108	AGTACACGCA GTGGGCGACG GATGGGGCTG AGTATGGGC CCATCCAGGC TAATCACACG	300
109		
110	GGCACAGGCC TGCTACTGAC CCTGCAGCCA GAACAGAAAGT TCCAGAAAGT GAAGGGATTT	360
111		
112	GGAGGGGCCA TGACAGATGC TGCTGCTCTC AACATCCTTG CCCTGTCACC CCCTGCCCAA	420
113		
114	AATTGCTAC TTAAATCGTA CTTCTCTGAA GAAGGAATCG GATATAACAT CATCCGGTA	480
115		
116	CCCATGGCCA GCTGTGACTT CTCCATCCGC ACCTACACCT ATGCAGACAC CCCTGATGAT	540
117		
118	TTCCAGTTGC ACAACTTCAG CCTCCCAGAG GAAGATACCA AGCTCAAGAT ACCCCTGATT	600
119		
120	CACCGAGCCC TGCAGTTGGC CCAGCGTCCC GTTCACTCC TTGCCAGCCC CTGGACATCA	660
121		
122	CCCACTTGGC TCAAGACCAA TGGAGCGGTG AATGGGAAGG CGTCACTCAA GGGACAGCCC	720
123		
124	GGAGACATCT ACCACCAGAC CTGGGCCAGA TACTTTGTGA AGTTCTGGA TGCCTATGCT	780
125		
126	GAGCACAAAGT TACAGTTCTG GGCAGTGACA GCTGAAAATG AGCCTTCTGC TGGGCTGTTG	840
127		
128	AGTGGATACC CCTTCCAGTG CCTGGCTTC ACCCCTGAAC ATCAGCGAGA CTTCATTGCC	900
129		
130	CGTGACCTAG GTCCTACCCCT CGCCAACAGT ACTCACCAACA ATGTCCGCCT ACTCATGCTG	960
131		
132	GATGACCAAC GCTTGCTGCT GCCCCACTGG GCAAAGGTGG TACTGACAGA CCCAGAACGA	1020
133		
134	GCTAAATATG TTCATGGCAT TGCTGTACAT TGGTACCTGG ACTTTCTGGC TCCAGCCAAA	1080
135		
136	GCCACCCCTAG GGGAGACACA CCGCCTGTTCC CCCAACACCA TGCTCTTGC CTCAGAGGCC	1140
137		
138	TGTGTGGGCT CCAAGTTCTG GGAGCAGAGT GTGCGGCTAG GCTCCTGGGA TCGAGGGATG	1200
139		
140	CAGTACAGCC ACAGCATCAT CACGAACCTC CTGTACCATG TGGTCGGCTG GACCGACTGG	1260
141		
142	AACCTTGCCC TGAACCCCCGA AGGAGGACCC AATTGGGTGC GTAACTTGT CGACAGTCCC	1320
143		
144	ATCATTGTAG ACGTCACCAG GGACACGTTT TACAAACAGC CCATGTTCTA CCACCTTGGC	1380
145		
146	CACTTCAGCA AGTTCATTCC TGAGGGCTCC CAGAGAGTGG GGCTGGTTGC CAGTCAGAAG	1440
147		
148	AACGACCTGG ACGCAGTGGC ACTGATGCAT CCCGATGGCT CTGCTGTTGT GGTCGTGCTA	1500
149		
150	AACCGCTCCT CTAAGGATGT GCCTCTTACC ATCAAGGATC CTGCTGTGGG CTTCCTGGAG	1560
151		
152	ACAATCTCAC CTGGCTACTC CATTACACCC TACCTGTGGC GTGCCAGAA TTCGGACTAC	1620

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/713,928ADATE: 12/31/96
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153
154 AAGGACGACG ATGACAAGTT GA 1642
155
156 (2) INFORMATION FOR SEQ ID NO:4:
157
158 (i) SEQUENCE CHARACTERISTICS:
159 (A) LENGTH: 546 amino acids
160 (B) TYPE: amino acid
161 (C) STRANDEDNESS: single
162 (D) TOPOLOGY: unknown
163
164 (ii) MOLECULE TYPE: peptide
165
166
167
168
169 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
170
171 Met Glu Phe Ser Ser Pro Ser Arg Glu Glu Cys Pro Lys Pro Leu Ser
172 1 5 10 15
173 Arg Val Ser Ile Met Ala Gly Ser Leu Thr Gly Leu Leu Leu Gln
174 20 25 30
175 Ala Val Ser Trp Ala Ser Gly Ala Arg Pro Cys Ile Pro Lys Ser Phe
176 35 40 45
177 Gly Tyr Ser Ser Val Val Cys Val Cys Asn Ala Thr Tyr Cys Asp Ser
178 50 55 60
179 Phe Asp Pro Pro Thr Phe Pro Ala Leu Gly Thr Phe Ser Arg Tyr Glu
180 65 70 75 80
181 Ser Thr Arg Ser Gly Arg Arg Met Glu Leu Ser Met Gly Pro Ile Gln
182 85 90 95
183 Ala Asn His Thr Gly Thr Gly Leu Leu Thr Leu Gln Pro Glu Gln
184 100 105 110
185 Lys Phe Gln Lys Val Lys Gly Phe Gly Gly Ala Met Thr Asp Ala Ala
186 115 120 125
187 Ala Leu Asn Ile Leu Ala Leu Ser Pro Pro Ala Gln Asn Leu Leu
188 130 135 140
189 Lys Ser Tyr Phe Ser Glu Glu Gly Ile Gly Tyr Asn Ile Ile Arg Val
190 145 150 155 160
191 Pro Met Ala Ser Cys Asp Phe Ser Ile Arg Thr Tyr Thr Tyr Ala Asp
192 165 170 175
193 Thr Pro Asp Asp Phe Gln Leu His Asn Phe Ser Leu Pro Glu Glu Asp
194 180 185 190
195

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206
207 Thr Lys Leu Lys Ile Pro Leu Ile His Arg Ala Leu Gln Leu Ala Gln
208 195 200 205
209
210 Arg Pro Val Ser Leu Leu Ala Ser Pro Trp Thr Ser Pro Thr Trp Leu
211 210 215 220
212
213 Lys Thr Asn Gly Ala Val Asn Gly Lys Gly Ser Leu Lys Gly Gln Pro
214 225 230 235 240
215
216 Gly Asp Ile Tyr His Gln Thr Trp Ala Arg Tyr Phe Val Lys Phe Leu
217 245 250 255
218
219 Asp Ala Tyr Ala Glu His Lys Leu Gln Phe Trp Ala Val Thr Ala Glu
220 260 265 270
221
222 Asn Glu Pro Ser Ala Gly Leu Leu Ser Gly Tyr Pro Phe Gln Cys Leu
223 275 280 285
224
225 Gly Phe Thr Pro Glu His Gln Arg Asp Phe Ile Ala Arg Asp Leu Gly
226 290 295 300
227
228 Pro Thr Leu Ala Asn Ser Thr His His Asn Val Arg Leu Leu Met Leu
229 305 310 315 320
230
231 Asp Asp Gln Arg Leu Leu Pro His Trp Ala Lys Val Val Leu Thr
232 325 330 335
233
234 Asp Pro Glu Ala Ala Lys Tyr Val His Gly Ile Ala Val His Trp Tyr
235 340 345 350
236
237 Leu Asp Phe Leu Ala Pro Ala Lys Ala Thr Leu Gly Glu Thr His Arg
238 355 360 365
239
240 Leu Phe Pro Asn Thr Met Leu Phe Ala Ser Glu Ala Cys Val Gly Ser
241 370 375 380
242
243 Lys Phe Trp Glu Gln Ser Val Arg Leu Gly Ser Trp Asp Arg Gly Met
244 385 390 395 400
245
246 Gln Tyr Ser His Ser Ile Ile Thr Asn Leu Leu Tyr His Val Val Gly
247 405 410 415
248
249 Trp Thr Asp Trp Asn Leu Ala Leu Asn Pro Glu Gly Gly Pro Asn Trp
250 420 425 430
251
252 Val Arg Asn Phe Val Asp Ser Pro Ile Ile Val Asp Val Thr Lys Asp
253 435 440 445
254
255 Thr Phe Tyr Lys Gln Pro Met Phe Tyr His Leu Gly His Phe Ser Lys
256 450 455 460
257
258 Phe Ile Pro Glu Gly Ser Gln Arg Val Gly Leu Val Ala Ser Gln Lys

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**SEQUENCE VERIFICATION REPORT
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Original Text